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NEWS 26 AUG 27 CAS definition of basic patents expanded to ensure comprehensive access to substance and sequence information
NEWS 27 SEP 18 Support for STN Express, Versions 6.01 and earlier, to be discontinued
NEWS 28 SEP 25 CA/CAplus current-awareness alert options enhanced to accommodate supplemental CAS indexing of exemplified prophetic substances

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FILE COVERS 1907 - 25 Sep 2008 VOL 149 ISS 13
FILE LAST UPDATED: 24 Sep 2008 (20080924/ED)

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```
=> s RL5
L1        22 RL5

=> s L1 and protein
     2209230 PROTEIN
     1556269 PROTEINS
     2579496 PROTEIN
             (PROTEIN OR PROTEINS)
L2        16 L1 AND PROTEIN

=> s L2 and ulbp-2
          80 ULBP
          26 ULBPS
          88 ULBP
             (ULBP OR ULBPS)
     9771362 2
           9 ULBP-2
             (ULBP(W)2)
L3         0 L2 AND ULBP-2

=> s L2 and ulbp2
          57 ULBP2
L4         1 L2 AND ULBP2
```

=> d L4 bib abs 1

L4 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:220357 CAPLUS
DN 140:269520
TI Cloning and characterization of a new human tumor marker RL5 and therapeutic use thereof
IN Wu, Jun; Luo, Ying
PA Shanghai Genomics, Inc., Peop. Rep. China
SO PCT Int. Appl., 33 pp.
CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2004022589	A1	20040318	WO 2002-CN631	20020909
WO 2004022589	A9	20050428		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002335297	A1	20040329	AU 2002-335297	20020909
CN 1668640	A	20050914	CN 2002-829568	20020909
CN 100358918	C	20080102		
US 20070275419	A1	20071129	US 2005-527257	20050309
PRAI WO 2002-CN631	A	20020909		

AB The present invention relates to a new tumor marker RL5 protein, which is transmembrane protein widely expressed in tumor tissues and cell lines but not expressed or expressed very low in normal tissues. Specifically, disclosed are the protein and cDNA sequence for RL5. The RL5 gene was mapped on chromosome 6q25.1 and its tumor expression profile is studied. RL5 has significant sequence homol. with another tumor marker ulbp2. Also provided are recombinantly expressed RL5 and antibodies to RL5. RL5 interacts in vivo with NKG2D receptor. The present invention also discloses the use of the RL5 proteins and the polynucleotides encoding them, e.g., diagnosing and treating for tumor. The present invention provides pharmaceutical compns. contg. the RL5 protein or the

antibody against it.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

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=> d L15 bib abs 1-16
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=> d L2 bib abs 1-16

L2 ANSWER 1 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2008:142296 CAPLUS
DN 148:512395
TI Engineering redox-sensitive linkers for genetically encoded FRET-based biosensors
AU Kolossov, Vladimir L.; Spring, Bryan Q.; Sokolowski, Anna; Conour, John E.; Clegg, Robert M.; Kenis, Paul J. A.; Gaskins, H. Rex
CS Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL, 61801, USA
SO Experimental Biology and Medicine (Maywood, NJ, United States) (2008), 233(2), 238-248
CODEN: EBMMBE; ISSN: 1535-3702
PB Society for Experimental Biology and Medicine
DT Journal
LA English
AB The ability to sense intracellular or intraorganellar redn./oxidn. conditions would provide a powerful tool for studying normal cell proliferation, differentiation, and apoptosis. Genetically encoded biosensors enable monitoring of the intracellular redox environment. We report the development of chimeric polypeptides useful as redox-sensitive linkers in conjunction with Forster resonance energy transfer (FRET). .alpha.-Helical linkers differing in length were combined with motifs that are sensitive to the redox state of the environment. The first category of linkers included a redox motif found in the thioredoxin family of oxidoreductases. This motif was flanked by two .alpha.-helixes of equal length. The second and third categories of redox linkers were composed of .alpha.-helixes with embedded adjacent and dispersed vicinal cysteine residues, resp. The linkers contg. redox switches were placed between a

FRET pair of enhanced cyan and yellow fluorescent proteins and these constructs were tested subsequently for their efficacy. A robust method of FRET anal., the (ratio)A method, was used. This method uses two fluorescence spectra performed directly on the FRET construct without phys. sepn. of the fluorophores. The cyan/yellow construct carrying one of the designed redox linkers, RL5, exhibited a 92% increase in FRET efficiency from its reduced to oxidized states. Responsiveness of the cyan-RL5-yellow construct to changes in the intracellular redox environment was confirmed in mammalian cells by flow cytometry.

RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN

AN 2007:968220 CAPLUS

DN 147:317026

TI Cloning, sequence and industrial applications of DUF152 domain-containing RL5 laccase from bovine rumen microflora metagenome and its homologs

IN Stroempl, Carsten; Golyshin, Peter; Ferrer, Manuel; Chernikova, Tatyana; Golyshina, Olga; Timmis, Kenneth; Elborough, Kieran; Jarvis, Graeme

PA Vialactia Biosciences (NZ) Limited, N. Z.; Helmholtz-Zentrum fuer Infektionsforschung G.m.b.H.

SO PCT Int. Appl., 111pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2007096184	A1	20070830	WO 2007-EP1589	20070223

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW

RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

EP 1826266	A1	20070829	EP 2006-3721	20060223

R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LI, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, AL,

BA, HR, MK, YU
AU 2007217715 A1 20070830 AU 2007-217715 20070223
PRAI EP 2006-3721 A 20060223
WO 2007-EP1589 W 20070223
AB The invention relates to a new laccase from rumen, namely the RL5 laccase. In particular, a metagenome library of bovine rumen microflora was constructed and a bacteriophage .lambda.-based expression library was established from DNA extd. from bovine rumen fluid. The expression library was screened for laccase activity and a gene encoding the inventive polypeptide with laccase activity, named RL5, without significant homol. to any known enzymes of this function, was isolated. This inventive RL5 laccase was identified as a protein , which is related to a major class of conserved (hypothetical) proteins contg. a so-called DUF152 domain of unknown function. The catalytic activity of the inventive RL5 laccase was analyzed and recombinant expression in E. coli unambiguously demonstrated its oxidizing multipotency for a variety of laccase substrates at an unusually broad pH range: from 3.5 to 9.0. Protein sequences of RL5 laccase homologs from various microbial sources are also disclosed. Furthermore, the invention relates to methods for producing inventive polypeptides and their use. The laccase of the present invention may be used as a food additive, for the textile, pulp and paper treatment and for environment protection.
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2006:781043 CAPLUS
DN 145:391195
TI Novel Polyphenol Oxidase Mined from a Metagenome Expression Library of Bovine Rumen: biochemical properties, structural analysis, and phylogenetic relationships
AU Beloqui, Ana; Pita, Marcos; Polaina, Julio; Martinez-Arias, Arturo; Golyshina, Olga V.; Zumarraga, Miren; Yakimov, Michail M.; Garcia-Arellano, Humberto; Alcalde, Miguel; Fernandez, Victor M.; Elborough, Kieran; Andreu, Jose M.; Ballesteros, Antonio; Plou, Francisco J.; Timmis, Kenneth N.; Ferrer, Manuel; Golyshin, Peter N.
CS Institute of Catalysis Cantoblanco, Consejo Superior de Investigaciones Cientificas (CSIC), Madrid, 28049, Spain
SO Journal of Biological Chemistry (2006), 281(32), 22933-22942
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB RL5, a gene coding for a novel polyphenol oxidase, was

identified through activity screening of a metagenome expression library from bovine rumen microflora. Characterization of the recombinant protein produced in Escherichia coli revealed a multipotent capacity to oxidize a wide range of substrates (syringaldazine >2,6-dimethoxyphenol > veratryl alc. > guaiacol > tetramethylbenzidine >4-methoxybenzyl alc. >2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonic acid) (ABTS) >> phenol red) over an unusually broad range of pH from 3.5 to 9.0. Apparent Km and kcat values for ABTS, syringaldazine, and 2,6-dimethoxyphenol obtained from steady-state kinetic measurements performed at 40.degree., pH 4.5, yielded values of 26, 0.43, and 0.45 .mu.M and 18, 660, and 1175 s-1, resp. The Km values for syringaldazine and 2,6-dimethoxyphenol are up to 5 times lower, and the kcat values up to 40 times higher, than values previously reported for this class of enzyme. RL5 is a 4-copper oxidase with oxidn. potential values of 745, 400, and 500 mV vs. normal hydrogen electrode for the T1, T2, and T3 copper sites. A three-dimensional model of RL5 and site-directed mutants were generated to identify the copper ligands. Bioinformatic anal. of the gene sequence and the sequences and contexts of neighboring genes suggested a tentative phylogenetic assignment to the genus BACTEROIDES: Kinetic, electrochem., and EPR analyses provide unequivocal evidence that the hypothetical proteins from Bacteroides thetaiotaomicron and from E. coli, which are closely related to the deduced protein encoded by the RL5 gene, are also multicopper proteins with polyphenol oxidase activity. The present study shows that these three newly characterized enzymes form a new family of functional multicopper oxidases with laccase activity related to conserved hypothetical proteins harboring the domain of unknown function DUF152 and suggests that some other of these proteins may also be laccases.

RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN

AN 2005:1314101 CAPLUS

DN 144:68263

TI Genes showing altered levels of expression in drug-resistant leukemia and their use in diagnosis and selection of drug target for therapy

IN Evans, William E.; Pieters, Rob; Cheok, Meyling H.; Den Boer, Monique L.; Yang, Wenjian

PA St. Jude Children's Research Hospital, USA; Erasmus University Medical Center Rotterdam

SO PCT Int. Appl., 124 pp.
CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2005118865	A2	20051215	WO 2005-US17424	20050518
WO 2005118865	A3	20060622		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2004-575762P P 20040528

AB The present invention encompasses methods and compns. useful in the diagnosis and treatment of drug resistant leukemia. The invention provides a no. of genes that are differentially expressed between drug resistant and drug sensitive acute lymphoblastic leukemia (ALL). These genes act as biomarkers for drug resistant leukemia, and further serve as mol. targets for drugs useful in treating drug resistant leukemia. Accordingly, the invention provides methods of diagnosing drug resistant leukemia and methods of selecting a therapy for subjects affected by drug-resistant leukemia. The invention also provides methods for screening for compds. for treating drug-resistant leukemia, and improved methods for treating drug-resistant leukemia. Compns. of the invention include arrays, computer readable media, and kits for use in the methods of the invention.

L2 ANSWER 5 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN

AN 2004:220357 CAPLUS

DN 140:269520

TI Cloning and characterization of a new human tumor marker RL5 and therapeutic use thereof

IN Wu, Jun; Luo, Ying

PA Shanghai Genomics, Inc., Peop. Rep. China

SO PCT Int. Appl., 33 pp.

CODEN: PIXXD2

DT Patent

LA Chinese

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

PI WO 2004022589 A1 20040318 WO 2002-CN631 20020909
WO 2004022589 A9 20050428
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
AU 2002335297 A1 20040329 AU 2002-335297 20020909
CN 1668640 A 20050914 CN 2002-829568 20020909
CN 100358918 C 20080102
US 20070275419 A1 20071129 US 2005-527257 20050309
PRAI WO 2002-CN631 A 20020909
AB The present invention relates to a new tumor marker RL5 protein, which is transmembrane protein widely expressed in tumor tissues and cell lines but not expressed or expressed very low in normal tissues. Specifically, disclosed are the protein and cDNA sequence for RL5. The RL5 gene was mapped on chromosome 6q25.1 and its tumor expression profile is studied. RL5 has significant sequence homol. with another tumor marker ulbp2. Also provided are recombinantly expressed RL5 and antibodies to RL5. RL5 interacts in vivo with NKG2D receptor. The present invention also discloses the use of the RL5 proteins and the polynucleotides encoding them, e.g., diagnosing and treating for tumor. The present invention provides pharmaceutical compns. contg. the RL5 protein or the antibody against it.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:499095 CAPLUS
DN 139:302562
TI Detection and identification of Legionella pneumophila by PCR-restriction fragment length polymorphism analysis of the RNA polymerase gene (rpoB)
AU Ko, Kwan Soo; Hong, Seong-Karp; Lee, Keun-Hwa; Lee, Hae Kyung; Park, Mi-Yeoun; Miyamoto, Hiroshi; Kook, Yoon-Hoh
CS SNUMRC, Institute of Endemic Diseases, Department of Microbiology and Cancer Research Institute, Seoul National University College of Medicine, Seoul, 110-799, S. Korea
SO Journal of Microbiological Methods (2003), 54(3), 325-337

CODEN: JMIMDQ; ISSN: 0167-7012
PB Elsevier Science B.V.
DT Journal
LA English
AB The partial RNA polymerase .beta.-subunit coding gene (rpoB) sequences of 38 Legionella species (59 ref. strains) were used to select both Legionella genus-specific and Legionella pneumophila species-specific primers to amplify the 347-bp and 217-bp DNAs, resp. Enzyme restriction sites for PCR-restriction fragment length polymorphism (PCR-RFLP) anal. were also generated by a computer program. Thirty-eight Legionella species were well differentiated by the identification scheme for Legionella genus-specific PCR-RFLP using HaeIII, AluI, CfoI, PstI, and MaeII. The most common and important pathogenic species, L. pneumophila, was differentiated into two subspecies (L. pneumophila pneumophila and L. pneumophila fraseri) by both Legionella genus-specific PCR-RFLP and L. pneumophila species-specific PCR-RFLP using BamHI. Eighty-two Korean culture isolates could also be easily identified by both PCR-RFLP methods as 68 strains of L. pneumophila pneumophila, 11 strains of L. pneumophila fraseri, and three novel strains that were sep. confirmed by 16S rDNA and rpoB sequence anal. These results suggest that the rpoB PCR-RFLP for Legionella is a simple and convenient method, not only for specific detection, but also for the rapid identification of Legionella species.
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2000:161466 CAPLUS
DN 132:204055
TI Production of clostridial toxins with recombinant cells producing rare codon-recognizing tRNAs
IN Zdanovsky, Alexey G.
PA Promega Corporation, USA
SO PCT Int. Appl., 69 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000012728	A1	20000309	WO 1999-US19284	19990823

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 6214602 B1 20010410 US 1998-143634 19980828

AU 9956885 A 20000321 AU 1999-56885 19990823

PRAI US 1998-143634 A 19980828

WO 1999-US19284 W 19990823

AB The present invention is directed to methods and compns. useful in the overprodn. of Clostridium toxins and proteins by hosts such as Escherichia coli. The host cell is genetically altered to produce tRNAs which recognize rare codons. These proteins and toxins find use in various medical and veterinary applications, including vaccine prodn., and cosmetic dermatol., as well as treatment of neurol. and other diseases and conditions. Thus, E. coli were transformed with plasmids contg. the ileX, argU and leuW genes and plasmids encoding Clostridium botulinum B, C and E toxins or C3 protein, iota toxin Ia protein of Clostridium perfringens, or tetanus toxin. Relative to wild-type E. coli, increased amts. of enzymically active toxins were produced by these transformants.

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN

AN 1998:620227 CAPLUS

DN 129:329621

OREF 129:67231a,67234a

TI Serp, an inhibitor of the interleukin-1.beta.-converting enzyme, is critical in the pathobiology of myxoma virus

AU Messud-Petit, Frederique; Gelfi, Jacqueline; Delverdier, Maxence; Amardeilh, Marie-France; Py, Robert; Sutter, Gerd; Bertagnoli, Stephane

CS Laboratoire Associe de Microbiologie Moleculaire, Institut National de la Recherche Agronomique and Ecole Nationale Veterinaire, Toulouse, F-31076, Fr.

SO Journal of Virology (1998), 72(10), 7830-7839
CODEN: JOVIAM; ISSN: 0022-538X

PB American Society for Microbiology

DT Journal

LA English

AB Recently, myxoma virus was shown to encode an addnl. member of the serpin superfamily. The viral gene, called serp2, was cloned, and the Serp2 protein was shown to specifically bind to interleukin-1.beta. (IL-1.beta.)-converting enzyme (ICE), thus inhibiting the cleavage of pro-IL-1.beta. by the protease (F. Petit, et al., 1996). Here, the authors address the role of Serp2 in the development of myxomatosis, a lethal infectious disease of the European rabbit. A Serp2 mutant myxoma

virus was constructed by disruption of the single-copy serp2 gene and insertion of the Escherichia coli gpt gene serving as the selectable marker. A revertant virus was obtained by replacing the E. coli gpt gene by the intact serp2 open reading frame. The Serp2- mutant virus replicated with wild-type kinetics both in rabbit fibroblasts and a rabbit CD4+ T-cell line (RL5). Moderate redn. of cell surface levels of major histocompatibility complex I was obsd. after infection with wild-type or Serp2- mutant myxoma virus, and both produced white pocks on the chorioallantoic membrane of the chick embryo. After the infection of European rabbits, the Serp2- mutant virus proved to be highly attenuated compared to wild-type myxoma virus, as demonstrated by the clin. course of myxomatosis and the survival rates of infected animals. Pathohistol. examns. revealed that infection with wild-type myxoma virus resulted in a blockade of the inflammatory response at the vascular level. In contrast, rapid inflammatory reactions occurred upon infection with the Serp2- mutant virus. Furthermore, lymphocytes in lymph nodes derived from animals inoculated with Serp2 mutant virus were shown to rapidly undergo apoptosis. The authors postulate that the virulence of myxoma virus in the European rabbit can be partially attributed to an impairment of host inflammatory processes and to the prevention of apoptosis in lymphocytes. The weakening of host defense is directly linked to serp2 gene function and is likely to involve the inhibition of IL-1.beta.-converting-enzyme-dependent pathways.

RE.CNT 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 9 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN

AN 1997:643177 CAPLUS

DN 127:289093

OREF 127:56369a,56372a

TI A ribosomal 5S rRNA-binding protein gene from rice (Oryza sativa) is regulated in a cell cycle phase-specific manner and in response to gibberellin

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CS Institut Allgemeine Botanik, Universitat Hamburg, Hamburg, D-22609, Germany

SO Journal of Plant Physiology (1997), 151(3), 334-338
CODEN: JPPHEY; ISSN: 0176-1617

PB Fischer

DT Journal

LA English

AB Transcripts of a ribosomal 5S rRNA-binding protein from rice (Oryza sativa), RL5, were shown to accumulate in internodes of deepwater rice after treatment with the growth-promoting hormone gibberellin (GA). Induction of RL5 expression by GA in the rice

internode was limited to the intercalary meristem and to the lower half of the elongation zone. Expression of RL5 was induced in G 1 phase of the cell cycle and reduced in abundance during S phase and again during mitosis. These results indicate that RL5 expression is highest in proliferating cells and is induced by mitotic stimulation. However, transcript levels are not consistently high in proliferating cells, but, instead, they are highly regulated during passage of cells through the different phases of the cell division cycle.

L2 ANSWER 10 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1997:304525 CAPLUS
DN 126:342191
OREF 126:66527a,66530a
TI Identification of the RI5.3 cDNA encoding polypeptide as the 7H6 antigen in rat tissues
AU Kuwahara, Kazuhide; Kokai, Yasuo
CS Dep. Pathol., Sapporo Med. Univ. Sch. Med., Japan
SO Sapporo Igaku Zasshi (1996), 65(6), 543-550
CODEN: SIZSAR; ISSN: 0036-472X
PB Sapporo Ika Daigaku
DT Journal
LA Japanese
AB The 7H6 antigen was recently found in our lab., which localized at tight junctions of various tissues. Using the 7H6 monoclonal antibody, we screened several rat liver cDNA libraries and isolated at 5.3 Kb cDNA termed RL5.3. The nucleotide sequence of the RL5.3 cDNA revealed one open reading frame encoding the 130 kD polypeptide (p130) homologous to a putative mechanochem. motor protein belonging to the SMC family. RT-PCR was set using a combination of primers corresponding to the nucleotide sequences of RL5.3 cDNA. This anal. revealed the expression of specific 263 bp PCR products in the thymus, liver, kidney and lung, in which epithelial cells have been known to possess tight junctions. Several independent antibodies raised against synthetic oligopeptides and recombinant fusion proteins based on the amino acid sequences of the p130 were employed for the detection of p130 in the rat tissues. The immunofluorescent localization of antigens reacting with these antibodies was found to be characteristic of tight junctions and indistinguishable from that of the 7H6 antigen. Collectively, the p130 polypeptide encoded by the RL5.3 cDNA was shown to be identical to the 7H6 antigen.

L2 ANSWER 11 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1996:470458 CAPLUS
DN 125:134394
OREF 125:24985a,24988a
TI Isolation of cDNA encoding 7H6-reactive polypeptide defines a new class of

protein with .alpha.-helical coiled-coil structure and DA-box similar to yeast chromosomal segregation proteins

AU Ezoe, Eiri; Kokai, Yasuo; Konishi, Yasuhiro; Kuwahara, Kazuhide; Zhong, Yun; Enomoto, Katsuhiko; Sawada, Norimasa; Hirata, Koichi; Mori, Michio

CS School Medicine, Sapporo Medical University, Sapporo, 060, Japan

SO Tumor Research (1995), 30, 21-36
CODEN: TUREA6; ISSN: 0041-4093

PB Sapporo Medical College, Cancer Research Institute

DT Journal

LA English

AB 7H6 monoclonal antibody was recently developed in our lab. by immunizing mice with a bile canaliculus-rich fraction of the rat liver. The antibody reacted with a novel 155 Kd polypeptide designated 7H6 antigen that specifically localizes at tight junctions of various epithelia. Correlations of the paracellular barrier function of the tight junction with expression of the 7H6 antigen at the cell border have suggested important roles of this polypeptide for the maintenance of tight junctional functions. As the first step for the anal. of the antigen at the mol. level, we isolated a series of cDNA clones encoding 7H6-reactive polypeptides. Five clones were isolated by immunoscreening. Among them a clone designated RL5.3 which carries the largest 5.3Kb insert was characterized in this study. Both plaque screening and immunoblotting of the fusion protein produced by the RL5.3 clone with lysogen confirmed that the protein specifically reacts with the 7H6 monoclonal antibody. Studies of cDNA clones showed that they were derived from a single class of transcripts. A partial sequence identified one open reading frame with an .alpha.-helical coiled coil structure and highly conserved aspartate (D)-Alanine residues with a helix-loop-helix structure correspond to the DA box. Since this domain has been specifically found in yeast chromosomal segregation proteins, the polypeptide encoded by the RL5.3 clone provides the first rodent counterpart of this protein family.

L2 ANSWER 12 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN

AN 1996:358305 CAPLUS

DN 125:77909

OREF 125:14643a,14646a

TI Disruption of M-T5, a novel myxoma virus gene member of the poxvirus host range superfamily, results in dramatic attenuation of myxomatosis in infected European rabbits

AU Mossman, Karen; Lee, Siow Fong; Barry, Michele; Boshkov, Lynn; McFadden, Grant

CS Dep. Biochem., Univ. Alberta, Edmonton, AB, T6G 2H7, Can.

SO Journal of Virology (1996), 70(7), 4394-4410
CODEN: JOVIAM; ISSN: 0022-538X

PB American Society for Microbiology

DT Journal
LA English
AB Myxoma virus is a pathogenic poxvirus that induces a lethal myxomatosis disease profile in European rabbits, which is characterized by fulminating lesions at the primary site of inoculation, rapid dissemination to secondary internal organs and peripheral external sites, and supervening gram-neg. bacterial infection. Here we describe the role of a novel myxoma virus protein encoded by the M-T5 open reading frame during pathogenesis. The myxoma virus M-T5 protein possesses no significant sequence homol. to nonviral proteins but is a member of a larger poxviral superfamily designated host range proteins. An M-T5- mutant virus was constructed by disruption of both copies of the M-T5 gene followed by insertion of the selectable marker p7.5Ecogpt. Although the M-T5- deletion mutant replicated with wild-type kinetics in rabbit fibroblasts, infection of a rabbit CD4+ T-cell line (RL5) with the myxoma virus M-T5- mutant virus resulted in the rapid and complete cessation of both host and viral protein synthesis, accompanied by the manifestation of all the classical features of programmed cell death. Infection of primary rabbit peripheral mononuclear cells with the myxoma virus M-T5- mutant virus resulted in the apoptotic death of nonadherent lymphocytes but not adherent monocytes. Within the European rabbit, disruption of the M-T5 open reading frame caused a dramatic attenuation of the rapidly lethal myxomatosis infection, and none of the infected rabbits displayed any of the characteristics features of myxomatosis. The two most significant histol. observations in rabbits infected with the M-T5- mutant virus were (i) the lack of progression of the infection past the primary site of inoculation, coupled with the establishment of a rapid and effective inflammatory reaction, and (ii) the inability of the virus to initiate a cellular reaction within secondary immune organs. We conclude that M-T5 functions as a crit. virulence factor by allowing productive infection of immune cells such as peripheral lymphocytes, thus facilitating virus dissemination to secondary tissue sites via the lymphatic channels.

L2 ANSWER 13 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1996:171414 CAPLUS
DN 124:256575
OREF 124:47469a,47472a
TI Genetic organization, size, and complete sequence of early region 3 genes of human adenovirus type 41
AU Yeh, Hung-Yueh; Pieniazek, Norman; Pieniazek, Danuta; Luftig, Ronald B.
CS Department Microbiology, Louisiana State University Medical Center, New Orleans, LA, 70112, USA
SO Journal of Virology (1996), 70(4), 2658-63
CODEN: JOVIAM; ISSN: 0022-538X
PB American Society for Microbiology

DT Journal
LA English
AB The complete nucleotide and predicted amino acid sequences for open reading frames (ORFs) of the human adenovirus type 41 (Ad41) early region 3 (E3) gene have been detd. The sequence of the Ad41 E3 gene (map units 74 to 83.9) consists of 3,373 nucleotides and has one TATA box and two polyadenylation signals (AATAAA). Anal. of the nucleotide sequence reveals that the E3 gene can encode six ORFs, designated RL1 to RL6. These are all expressed at the mRNA level, as detd. by reverse transcription-PCR anal. of Ad41-infected cell RNA. When compared with known E3 sequences of most other human adenoviruses deposited in GenBank, the sequences of RL1 to RL3 were found to be unique to subgroup F adenoviruses (Ad40 and Ad41). They encode putative proteins of 173 amino acids (19.4 kDa) and 276 amino acids (31.6 kDa) in one reading frame as well as a 59-amino-acid (6.7 kDa) protein in an overlapping reading frame. RL4 encodes a 90-amino-acid protein (10.1 kDa) with 40% homol. to the Ad2 E3 10.4-kDa protein, which induces degrdn. of the epidermal growth factor receptor and functions together with the Ad2 E3 14.5-kDa protein to protect mouse cell lines against lysis. RL5 encodes a protein of 107 amino acid residues (12.3 kDa) and is analogous to the Ad2 E3 14.5-kDa protein. RL6 codes for a protein of 122 amino acids (14.7 kDa) that is analogous to the Ad2 14.7-kDa protein, which functions to protect Ad-infected cells from tumor necrosis factor-induced cytolysis. This finding of three unique (RL1 to RL3) E3 gene ORFs may explain why subgroup F adenoviruses differ substantially from other human adenoviruses in their host range; i.e., they replicate predominantly in the host's gastrointestinal rather than respiratory tract. A recent phylogenetic study that compared subgroup F Ad40 DNA sequences with representatives of subgroups B (Ad3), C (Ad2), and E (Ad4) reached a similar conclusion about the uniqueness of RL1 and RL2.

L2 ANSWER 14 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1995:793442 CAPLUS
DN 124:2002
OREF 124:451a,454a
TI Rice 5S ribosomal RNA and its binding protein genes: structure and expression
AU Kim, Ju-Kon; Hahm, Baek Hie
CS Dep. Genetic Eng., Univ. Suwon, Suwon, 440-600, S. Korea
SO Molecules and Cells (1995), 5(4), 381-7
CODEN: MOCEEK; ISSN: 1016-8478
PB Korean Society of Molecular Biology
DT Journal
LA English
AB The authors have isolated a genomic clone contg. rice 5 S rRNA

(rRNA-encoding) genes (rDNA). The clone contains 10 repeat units of 290 bp, plus 2.0 kb of flanking genomic sequence at one border. Sequencing of individual repeat units shows that the sequence of the 5 S rRNA coding region is very similar to that reported for other flowering plants, while the nontranscribed spacer region is diverged. Genomic DNA-blot anal. indicates that 5 S rDNA occurs in long tandem arrays. A rice 5 S rRNA-binding protein gene (RL5) was previously isolated and sequenced [Kim, J.-K., and Wu, R (1993) Plant Mol. Biol. 23, 409-413]. Amino acid sequence anal. of the RL5 protein revealed that it has many intriguing features. These include the presence of three repeated amino acid sequences and the conservation of glycine residues, which may be important for 5 S rRNA/RL5 protein interactions. Genomic DNA-blot anal. indicates that there are fewer copies of the RL5 gene in rice than in other eukaryotes. The RL5 gene appears to be constitutively expressed at high levels in rice tissues.

L2 ANSWER 15 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1995:301849 CAPLUS
DN 122:309029
OREF 122:56077a,56080a
TI Cloning and expression of a cDNA encoding a cytoplasmic L5 ribosomal protein from alfalfa (Medicago sativa L.)
AU Asemota, Omorefe; Breda, Colette; Sallaud, Christophe; El Turk, Joumana; de Kozak, Isabelle; Buffard, Dominique; Esnault, Robert; Kondorosi, Adam
CS Institut des Sciences Vegetales, CNRS, Gif sur Yvette, 91198, Fr.
SO Plant Molecular Biology (1994), 26(4), 1202-5
CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
AB A cDNA encoding a putative cytoplasmic ribosomal protein L5 from alfalfa (MsRL5), the first sequence from higher plants, has been characterized. The derived amino acid sequence of 181 residues contains the L5 signature, is 72.2% identical to yeast ribosomal L5 and shares high identity with other RL5 peptides from eukaryotic origin. The sequence does not contain any signal or transit peptide and therefore might be cytoplasmic. In all alfalfa organs examd. MsRL5 transcripts were detected at approx. equal levels.

L2 ANSWER 16 OF 16 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1979:435604 CAPLUS
DN 91:35604
OREF 91:5791a,5794a
TI Light effects in yeast: evidence for participation of cytochromes in photoinhibition of growth and transport in Saccharomyces cerevisiae

cultured at low temperatures

AU Ulaszewski, Stanislaw; Mamouneas, Theofanis; Shen, Win-Kuang; Rosenthal, Philip J.; Woodward, John R.; Cirillo, Vincent P.; Edmunds, Leland N., Jr.

CS Dep. Biochem., State Univ. New York, Stony Brook, NY, 11794, USA

SO Journal of Bacteriology (1979), 138(2), 523-9

CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AB Visible light of moderate intensity inhibits growth, respiration, protein synthesis, and membrane transport in bakers' yeast and has a deleterious effect on membrane integrity. These effects required cytochromes b and a/a3. The light sensitivities of growth rate and histidine-14C uptake in wild-type rho+ Y185 and D225-5A strains of S. cerevisiae were compared with those in a variety of mutants lacking cytochrome b or a/a3 or both; a close correlation was found between the presence of these respiratory pigments and photosensitivity. Thus, strain RL5-3C, a nuclear petite lacking cytochromes b, a, and a3, was resistant to light; strain GL5-6A, another nuclear petite having reduced amts. of cytochromes a and a3, was partially resistant; strains MB127-20C and MB1-6C, nuclear petites lacking only cytochrome b, were also partially resistant to light; whereas mutants contg. all 3 cytochromes but having their respiratory chain either nonfunctional (strain ZK3-6B) or uncoupled (strain 18-27t12) were fully sensitive to light. An equal-energy, broad-band action spectrum for the light inhibition of growth and transport indicated that blue light (408 nm) was most effective; these wavelengths correspond to the Soret region of the cytochrome absorption spectrum. Apparently, yeast cytochromes b, a, and a3 are the primary photoreceptors for the inhibitory effect of light and, perhaps, for other processes, such as the entrainment of biol. rhythms in this species.